

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SAGAWA, HIROAKI  
          UENO, HARUMI  
          OSHIMA, ATSUSHI  
          KATO, IKUNOSHIN
- (ii) TITLE OF INVENTION: PLASMID
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
  - (B) STREET: PO BOX 747
  - (C) CITY: FALLS CHURCH
  - (D) STATE: VA
  - (E) COUNTRY: USA
  - (F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: WEINER, MARC S.
  - (B) REGISTRATION NUMBER: 32,181
  - (C) REFERENCE/DOCKET NUMBER: 1422-0319P
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 703-205-8000
  - (B) TELEFAX: 703-205-8050

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 295 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 2
  - (D) OTHER INFORMATION: /note= "2=Val or Leu"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Xaa	Pro	Leu	Asp	Lys	Asp	Leu	Gln	Lys	Ala	Lys	Ile	Ser	Ile	Thr	1	5	10	15
Asp	Phe	Phe	Glu	Ile	Thr	Asn	Arg	Val	Leu	Asp	Tyr	Phe	Pro	Asn	Val	20	25	30	
Ile	Asn	Asn	Thr	Val	Glu	Lys	Gly	Asp	Tyr	Leu	Ile	Ser	Ser	Ser	Asn	35	40	45	
Ile	Ala	Gly	Thr	Ile	Lys	Phe	Leu	Arg	Pro	Ile	Asn	Arg	Lys	Leu	Phe	50	55	60	
Ile	Gln	Glu	Lys	Lys	Val	Phe	Asn	Asp	Tyr	Phe	Gln	Lys	Leu	Ile	Ile	65	70	75	80
Val	Phe	Glu	Asn	Ile	Arg	Asn	Lys	Lys	Thr	Val	Thr	Glu	Glu	Asp	Lys	85	90	95	
Ile	Ile	Ile	Asp	Arg	Val	Ile	Tyr	Thr	Ile	Gln	Gln	Ser	Ile	Gly	Ile	100	105	110	
Gly	Leu	Asp	Leu	Met	Val	Asn	Gln	Asn	Ser	Ala	Arg	Lys	His	Val	Gly	115	120	125	
Asn	Arg	Phe	Glu	Glu	Leu	Ile	Arg	Val	Ile	Phe	Thr	Glu	Ile	Ser	Val	130	135	140	
Ser	Asn	Lys	Arg	Thr	Val	Leu	Gln	Ile	Pro	Tyr	Glu	Thr	Asp	Glu	Gly	145	150	155	160
Gln	Lys	Ile	Tyr	Lys	Cys	Glu	Asn	Asp	Leu	Ile	Ile	Ser	Pro	Phe	Glu	165	170	175	
Asn	Val	Glu	Ser	Thr	Asn	Lys	His	Leu	Asp	Glu	Asn	Glu	Ile	Val	Val	180	185	190	
Ser	Ile	Lys	Thr	Thr	Ser	Lys	Asp	Arg	Met	Gly	Lys	Met	Phe	Ile	Asp	195	200	205	
Lys	Ile	Leu	Leu	Glu	Arg	Phe	Val	Lys	His	Pro	Gln	Lys	Val	Ile	Gly	210	215	220	
Ile	Phe	Leu	Asn	Asp	Val	Gln	Arg	Lys	Glu	Asp	Asn	Asn	Ile	Ser	Phe	225	230	235	240
Thr	Leu	Val	Ser	Gly	Leu	Phe	Met	Val	Tyr	Thr	Lys	Phe	Leu	Thr	Thr	245	250	255	
Leu	Glu	Gly	Ile	Tyr	Tyr	Leu	Asp	Pro	Pro	Pro	Asn	Ala	Leu	Lys	Leu	260	265	270	
Pro	Tyr	Ser	Asn	His	Met	Lys	Arg	Phe	Ser	Asp	Leu	Ile	Thr	Glu	Asp	275	280	285	
Leu	Glu	Lys	Leu	Phe	Ser	Ser	290	295											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGSTACCAC TGGATAAAGA TTTACAAAAA GCAAAGATTT CAATTACTGA TTTTTTTGAA	60
ATTACAAATA GAGTTTTAGA TTATTTCCCC AATGTAATCA ATAATACAGT TGAAAAAGGA	120
GATTATTTAA TATCCTCATC AAATATTGCT GGAACAATAA AATTCCTAAG ACCAATCAAT	180
AGAAAGTTAT TTATTCAGGA AAAAAAAGTT TTCAATGATT ATTTTCAAAA ACTGATTATA	240
GTTTTTGAAA ATATAAGGAA CAAAAAACT GTAACAGAGG AAGATAAAAT TATTATTGAT	300
AGGGTAATTT ACACAATACA GCAATCTATT GGAATTGGTT TAGATTTAAT GGTTAATCAA	360
AATAGTGCTA GAAAGCACGT TGGTAACCGA TTTGAAGAAT TAATTAGAGT CATTTTTACA	420
GAAATATCAG TATCGAATAA AAGAACTGTA TTACAAATTC CATATGAAAC TGATGAAGGA	480
CAGAAAATTT ACAAATGCGA GAATGACCTC ATTATTTCTC CTTTTGAAAA TGTAGAATCT	540
ACAAACAAAC ATCTAGATGA AAATGAGATT GTTGTTCAT TAAAGACAAC ATCAAAAGAT	600
AGGATGGGAA AAATGTTTAT AGATAAAATT TTAAGTAAAA GGTTCGTTAA ACACCTCAA	660
AAAGTTATAG GGATTTTCCT CAATGATGTA CAAAGAAAAG AAGACAACAA TATCAGCTTT	720
ACACTTGTTT CAGGATTATT TATGGTGTAT ACTAAATTCT TAACTACTCT TGAAGGGATC	780
TATTATTTAG ATCCACCACC TAATGCATTG AAATACCAT ATTCTAATCA TATGAAAAGA	840
TTTTCAGATT TAATTACAGA AGACCTTGAA AAATTATTCT CCTCT	885

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TATGGATATG TTCATAAACA CGCATGTAGG CAGATAGATC TTTGGTTGTG AATCGCAACC	60
AGTGGCCTTA TGGCAGGAGC CGCGGATCAC CTACCATCCC TAATGACCTG CAGGCATGCA	120

AGCTTGCATG CCTGCAGGTC ATTAGGTACG GCAGGTGTGC TCGAGGCGAA GGAGTGCCTG 180  
 CATGCGTTTC TCCTTGGCTT TTTTCCTCTG GGACA 215

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TATGTCCCAG AGGAAAAAAG CCAAGGAGAA ACGCATGCAG GCACTCCTTC GCCTCGAGCA 60  
 CACCTGCCGT ACCTAATGAC CTGCAGGCAT GCAAGCTTGC ATGCCTGCAG GTCATTAGGG 120  
 ATGGTAGGTG ATCCGCGGCT CCTGCCATAA GGCCACTGGT TCGGATTAC AACCAAAGAT 180  
 CTATCTGCCT ACATGCGTGT TTATGAACAT ATCCA 215

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGATCTAGAG CAAACAAAAA AACCACCG 28

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTCTAGATC CCAGAGGAAA AAAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCGAGATTT AGGTGACACT ATAGAATACG GAATTGTGAG CGGATAACAA TTCCAAGCTT 60

CACAGGAAAC AGACCATGGC TTAAGTAACT AGTGAATTCG 100

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGAATTCACT AGTTACTTAA GCCATGGTCT GTTCCTGTG AAGCTTGGAA TTGTTATCCG 60

CTCACAATTC CGTATTCTAT AGTGTCACCT AAATCTCGAG 100

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATCCCATGG AACGCTACGA ATCTCTG

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGCCATGG TTATTTTGA CACCAGACC

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAACTTGAAT CCATGGGTTC TCACCG

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TACTCAGTAG CCATGGCTCT CATAGACCG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Asn	Glu	Ile	Ala	Phe	Asp	Asn	Tyr	Ser	Tyr	Ile	Pro	Lys	Leu	Lys	
1				5					10					15		
Leu	Tyr	Ser	Glu	Ile	Glu	Leu	Lys	Pro	Phe	Phe	Ile	Ser	Lys	Asn	Gly	
			20					25					30			
Ser	Leu	Phe	Asn	Val	Asp	Ala	Ile	Asp	Phe	Leu	Arg	Lys	Leu	Glu	Ser	
		35					40					45				
Asn	Ser	Val	Asp	Leu	Ile	Phe	Ala	Asp	Pro	Pro	Tyr	Asn	Ile	Lys	Lys	
	50					55					60					
Ala	Glu	Trp	Asp	Ile	Phe	Ser	Ser	Gln	Asn	Glu	Tyr	Leu	Glu	Trp	Ser	
65				70					75					80		
Lys	Glu	Trp	Ile	Met	Glu	Ala	His	Arg	Val	Leu	Lys	Asp	Asn	Gly	Ser	
			85					90						95		
Leu	Tyr	Val	Cys	Gly	Phe	Ser	Glu	Ile	Leu	Ala	Asp	Ile	Lys	Phe	Ile	
		100						105					110			
Thr	Ser	Lys	Tyr	Phe	His	Ser	Cys	Lys	Trp	Leu	Ile	Trp	Phe	Tyr	Arg	
		115					120					125				
Asn	Lys	Ala	Asn	Leu	Gly	Lys	Asp	Trp	Gly	Arg	Ser	His	Glu	Ser	Ile	
	130					135					140					
Leu	Leu	Leu	Arg	Lys	Ser	Lys	Asn	Phe	Ile	Phe	Asn	Ile	Asp	Glu	Ala	
145				150						155				160		
Arg	Ile	Pro	Tyr	Asn	Glu	His	Thr	Val	Lys	Tyr	Pro	Gln	Arg	Thr	Gln	
			165					170					175			
Ala	Glu	Ser	Ser	Gln	Tyr	Ser	Asn	Ser	Lys	Lys	Gln	Tyr	Ile	Trp	Glu	
		180					185						190			
Pro	Asn	Pro	Leu	Gly	Ala	Lys	Pro	Lys	Asp	Val	Leu	Glu	Ile	Pro	Thr	
		195					200					205				
Ile	Ser	Asn	Gly	Ser	Trp	Glu	Arg	Ser	Ile	His	Pro	Thr	Gln	Lys	Pro	
	210					215				220						
Val	Glu	Leu	Leu	Lys	Lys	Ile	Ile	Leu	Ser	Ser	Ser	Asn	Lys	Asp	Ser	
225				230					235					240		
Leu	Ile	Leu	Asp	Pro	Phe	Gly	Gly	Ser	Gly	Thr	Thr	Tyr	Ala	Val	Ala	
			245					250					255			
Glu	Ala	Phe	Gly	Arg	Lys	Trp	Ile	Gly	Thr	Glu	Leu	Asp	Lys	Asn	Tyr	
		260					265					270				
Cys	Leu	Glu	Ile	Gln	Lys	Arg	Leu	Lys	Asp	Glu	Ser	Met	Ile	Asn	Arg	

Ile Phe Ser Gly Asp Asp Asp Ser Asn Ser Gln Asn Arg Arg Lys Lys  
 290 295 300

Leu Arg Gly Glu  
 305

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAATGAAA TAGCGTTTGA TAATTACAGT TATATACCAA AATTAAAACT TTATTCGGAA	60
ATCGAGCTTA AACCATTTTT TATTTCAAAA AACGGTTCAC TTTTCAATGT TGATGCTATT	120
GATTTTTTTAA GAAAATTAGA GAGTAATTCT GTGGATTTAA TTTTGCAGA TCCACCTTAT	180
AACATTAAAA AGGCAGAGTG GGATATTTTT TCTTCTCAAA ATGAATATCT CGAATGGAGT	240
AAAGAATGGA TAATGGAAGC TCATAGAGTT TAAAAGATA ATGGCAGTTT ATATGTTTGT	300
GGCTTTTCAG AAATTCTGGC AGACATAAAA TTTATCACTT CAAAATATTT TCACAGTTGT	360
AAATGGTTGA TTTGGTTCTA TAGAAACAAG GCAAATTTAG GTAAAGATTG GGGACGTTCA	420
CACGAAAGTA TACTGTTATT AAGAAAATCT AAAAATTTTA TTTTAAATAT TGATGAGGCA	480
CGAATCCCGT ATAATGAGCA TACAGTTAAA TATCCACAAA GAACCCAGGC CGAATCTTCG	540
CAATATTCGA ACTCAAAAAA GCAATATATT TGGGAGCCAA ACCCATTAGG AGCTAAGCCA	600
AAAGATGTTT TGGAGATTCC CACAATTTCA AATGGTTCTT GGGAAAGAAG TATTCACCCT	660
ACGCAAAAGC CAGTAGAATT GCTTAAAAAA ATAATTTTAT CTCATCTAA TAAAGATAGT	720
TTAATTCTTG ATCCATTTGG TGGTTCGGGA ACTACATATG CTGTTGCGGA AGCTTTTGGC	780
AGAAAATGGA TTGGAACAGA GTTAGATAAA AATTATTGTC TGGAAATTCA AAAGCGATTG	840
AAAGACGAAA GTATGATCAA CAGGATTTTT TCAGGCGATG ATGATTCAAA TTCTCAAAT	900
AGAAGAAAAA AATTAAGAGG AGAA	924

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGAGATTTA GGTGACACTA TAGAATACA

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGCTTGATT CTATAGTGTC ACCTAAATC

29

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCGAGATTTA GGTGACACTA TAGAATACGG AATTGTGAGC GGATAACAAT TCCA

54

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCTTGGAAT TGTTATCCGC TCACAATTCC GTATTCTATA GTGTCACCTA AATC

54

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Leu	Pro	Leu	Asp	Lys	Asp	Leu	Gln	Lys	Ala	Lys	Ile	Ser	Ile	Thr
1				5				10					15		
Asp	Phe	Phe	Glu												
			20												

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: primer\_bind
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "6, 9, 12 = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGTTNCCNY TNGAYAARGA YYT

23

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY: primer\_bind  
(B) LOCATION: 1..23  
(D) OTHER INFORMATION: /note= "9 = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGGATTTNC ARAARGCNAA RAT

23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAAATCTAAA CCAATTCCAA TAGATTGCTG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAAATCTAAA CCAATTCCAA TAGATTGCTG

30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACAGAAAAT TTACAAATGC GAGAAATGACC

30

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCATGGCACA CGTTTCAAAA AAGAAATCCT CGAAGTCAAA TATGATGAGA AAAACATCTC	60
AGACATCCTG CATATGACGG TGGATGAAGC ATTGGAATTT TTCTCGGAAA ATCACGAAGA	120
AAAAATTGTA ACCAACTAA AACCTTTGCA GGACGTTGGT TTGGGTTATC TTCAGTTAGG	180
CCAGTCCTCC TCTACTCTTT CCGGCGGTGA AGCCCAAAGA GTGAAGCTCG CCTCTTTCCT	240
TGTGAAAGGT GTAACGACGG AAAAAACGTT ATTTGTTTTT GATGAACCAT CAACAGGATT	300
ACATTTCCAC GACATTCAAA AATTACTGAA ATCACTTCAG GCACTGATAG AATTAGGGCA	360
TTCGGTTGTA GTGATTGAGC ATCAGCCGGA TATTATCAAA TGCGCCGATT ACATCATCGA	420
TGTCGGACCC AATGCCGGA AATACGGTGG CGAAATTGTT TTCACAGGAA CTCCGGAAGA	480
TTTGGTAAAA GAGAAAAAGT CGTTTACAGG GAAGTATATT AAGGAGAAGT TAAAGTAATT	540
TATTTATATT TGAAGTTATG CTACCACTGG ATAAAGATTT ACAAAAAGCA AAGATTTCAA	600
TTACTGATTT TTTTGAAATT ACAAATAGAG TTTTAGATTA TTTCCCAAT GTAATCAATA	660
ATACAGTTGA AAAAGGAGAT TATTTAATAT CCTCATCAAA TATTGCTGGA ACAATAAAAT	720
TCCTAAGACC AATCAATAGA AAGTTATTTA TTCAGGAAAA AAAAGTTTTT AATGATTATT	780

TTCAAAACT GATTATAGTT TTTGAAAATA TAAGGAACAA AAAAAGTGT ACAGAGGAAG	840
ATAAAATTAT TATTGATAGG GTAATTTACA CAATACAGCA ATCTATTGGA ATTGGTTTAG	900
ATTTAATGGT TAATCAAAAT AGTGCTAGAA AGCACGTTGG TAACCGATTT GAAGAATTAA	960
TTAGAGTCAT TTTTACAGAA ATATCAGTAT CGAATAAAAG AACTGTATTA CAAATTCCAT	1020
ATGAAACTGA TGAAGGACAG AAAATTTACA AATGCGAGAA TGACCTCATT ATTTCTCCTT	1080
TTGAAAATGT AGAATCTACA AACAAACATC TAGATGAAAA TGAGATTGTT GTTTCATAA	1140
AGACAACATC AAAAGATAGG ATGGGAAAAA TGTTTATAGA TAAAATTTTA CTTGAAAGGT	1200
TTGTTAAACA CCCTCAAAAA GTTATAGGGA TTTTCCTCAA TGATGTACAA AGAAAAGAAG	1260
ACAACAATAT CAGCTTTACA CTTGTTTCAG GATTATTTAT GGTGTATACT AAATTCTTAA	1320
CTACTCTTGA AGGGATCTAT TATTTAGATC CACCACCTAA TGCATTGAAA CTACCATATT	1380
CTAATCATAT GAAAAGATTT TCAGATTTAA TTACAGAAGA CCTTGAAAAA TTATTCTCCT	1440
CTTAATTTTT TTCTTCTATT TTGAGAATTT GAATCATCAT CGCCTGAAAA AATCCTGTTG	1500
ATCATACTTT CGTCTTTCAA TCGCTTTTGA ATTTCCAGAC AATAATTTTT ATCTAACTCT	1560
GTTCCAATCC ATTTTCTGCC AAAAGCTT	1588

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATATTTGAAG CCATGGTACC ACTGG	25
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(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGATCTGGTC ATCCCAAACA AAAATCTTTC GGTTTACGAA GATGCAGTCG CTCCTGGAA	60
AGGCGAAAGT ATGAGCGAAT GGAAAAAGGA ATTCATCAAA AAAGCCAAAC ATTTCCCAAT	120
TCACAAGCCT TATCATCAAC TCACAAAAGA GCAGAAACAG TTCCTTTGGA AAGGCGATAA	180
AACCAGAAGT TTCCCAAGTA TTGATAATTT TTTCAAAATG CTTGAAGAGA ATCTTTACAA	240
GATCCAATAC CGCGTAATGC TTTGCGCTA TCGTGGGAAA AACTTTGCC CCGATTGCGA	300
AGGATTACGA TTGCGGGAAG AAACAAGCTG GGTGAAGATT GACGGACACA ACATTCAGTC	360
TTTGATTGAA TTACCTTTGG ATGAACTCCT GCCATTGATC AAAAGCTTAA AACTGAACGT	420
CCACGACAGA GAAATTGCCA AACGCCTGAC TTACGAAATC GAAACGAGAT TAGAATTCCT	480
GACGAAAGTC GGCCTTGAT ATCTGACTTT GAACCGAACA TCCAACACGC TTTCCGGAGG	540
AGAAAGCCAG AGAATCAATC TGGCGACAGC TTGGGAAGTT CGCTGGTTGG TTCTATTTAT	600
ATTTTGGATG AGCCGAGCAT TGGTCTGCAT TCCCGCGATA CAGAAAATCT GATTGGTGTC	660
CTCAAACAAC TCCGCGATTT GGGAANTACC GTGATTGTTG TAGAACACGA CGAAGATGTG	720
ATGCTTGCGG CAGNTTACAT TATAGATATT GGCCCNAG CGGGCTACCT TGGTGGCGAT	780
CTTGTTTTCA GCGNGGATTA TAAAGAGATG CTGAAGTNTN ATACTTTAAC CGCAAAATAC	840
CTGAATGGCG AACTGAAAAT AGAAGTTCCT GAAAAACGAA GAAAACCGAA GGAATTCATC	900
GCAATAAAAAG GTGCCCAGCA GAATAATTTA AAAAATATTG ACGTTGATGT TCCGTTAGAA	960
TGTCTGACAG TTATCACAGG CGTTTCTGGA AGCGGGAAAT CCACTTTGAT GAAGGAAGTG	1020
ATGACCAATG CCATCCAGAT CCAACTGGGA ATGGGCGGCA AAAAAGCCGA TTACGATTCTG	1080
GTGGAATTCC CGAAAAAGCT GATCCAGAAT ATCGAACTGA TTGACCAGAA CCAATCGGG	1140
AAATCGTCCC GCTCCAACCC CGTGACTTAT CTGAAAGCTT ACGACGATAT CCGGGATCTT	1200
TTTGCGAAAC AAAAATCCGC AAAAATCCAG GGTTACAAAC CGAAGCATTT CTCCTTCAAT	1260
GTGGATGGCG GAAGATGTGA CGAGTGCAAA GGCGAAGGTA TCATTACCGT ATCAATGCAG	1320

TTTATGGCGG	ACATCGAGCT	GGAGTGTGAG	CATTGCCATG	GCACACGTTT	CAAAAAAGAA	1380
ATCCTCGAAG	TCAAATATGA	TGAGAAAAAC	ATCTCAGACA	TCCTGCATAT	GACGGTGGAT	1440
GAAGCATTGG	AATTTTTCTC	GGAAAATCAC	GAAGAAAAAA	TTGTAACCAA	ACTAAAACCT	1500
TTGCAGGACG	TTGGTTTGGG	TTATCTTCAG	TTAGGCCAGT	CCTCCTCTAC	TCTTTCCGGC	1560
GGTGAAGCCC	AAAGAGTGAA	GCTCGCCTCT	TTCCTTGTA	AAGGTGTAAC	GACGGAAAAA	1620
ACGTTATTTG	TTTTTGATGA	ACCATCAACA	GGATTACATT	TCCACGACAT	TCAAAAATTA	1680
CTGAAATCAC	TTCAGGCACT	GATAGAATTA	GGGCATTCCG	TTGTAGTGAT	TGAGCATCAG	1740
CCGGATATTA	TCAAATGCGC	CGATTACATC	ATCGATGTCT	GACCCAATGC	CGGAAAATAC	1800
GGTGGCGAAA	TTGTTTTTAC	AGGAACTCCG	GAAGATTTGG	TAAAAGAGAA	AAAGTCGTTT	1860
ACAGGGGAAGT	ATATTAAGGA	GAAGTTAAAG	TAATTTATTT	ATATTTGAAG	TTATGCTACC	1920
ACTGGATAAA	GATTTACAAA	AAGCAAAGAT	TTCAATTACT	GATTTTTTTG	AAATTACAAA	1980
TAGAGTTTTA	GATTATTTCC	CCAATGTAAT	CAATAATACA	GTTGAAAAAG	GAGATTATTT	2040
AATATCCTCA	TCAAATATTG	CTGGAACAAT	AAAATTCCTA	AGACCAATCA	ATAGAAAGTT	2100
ATTTATTCAG	GAAAAAAAAG	TTTTCAATGA	TTATTTTCAA	AAACTGATTA	TAGTTTTTGA	2160
AAATATAAGG	AACAAAAAAA	CTGTAACAGA	GGAAGATAAA	ATTATTATTG	ATAGGGTAAT	2220
TTACACAATA	CAGCAATCTA	TTGGAATTGG	TTTAGATTTA	ATGGTTAATC	AAAATAGTGC	2280
TAGAAAGCAC	GTTGGTAACC	GATTTGAAGA	ATTAATTAGA	GTCATTTTTA	CAGAAATATC	2340
AGTATCGAAT	AAAAGAACTG	TATTACAAAT	TCCATATGAA	ACTGATGAAG	GACAGAAAAT	2400
TTACAAATGC	GAGAATGACC	TCATTATTTT	TCCTTTTGAA	AATGTAGAAT	CTACAAACAA	2460
ACATCTAGAT	GAAAATGAGA	TTGTTGTTTC	AATAAAGACA	ACATCAAAAG	ATAGGATGGG	2520
AAAAATGTTT	ATAGATAAAA	TTTTACTTGA	AAGGTTTGTT	AAACACCCTC	AAAAAGTTAT	2580
AGGGATTTTC	CTCAATGATG	TACAAAGAAA	AGAAGACAAC	AATATCAGCT	TTACACTTGT	2640
TTCAGGATTA	TTTATGGTGT	ATACTAAATT	CTTAECTACT	CTTGAAGGGA	TCTATTATTT	2700
AGATCCACCA	CCTAATGCAT	TGAAACTACC	ATATTCTAAT	CATATGAAAA	GATTTTCAGA	2760
TTTAATTACA	GAAGACCTTG	AAAAATTATT	CTCCTCTTAA	TTTTTTTCTT	CTATTTTGAG	2820
AATTTGAATC	ATCATCGCCT	GAAAAAATCC	TGTTGATCAT	ACTTTCGTCT	TTCAATCGCT	2880
TTTGAATTTT	CAGACAATAA	TTTTTATCTA	ACTCTGTTCC	AATCCATTTT	CTGCCAAAAG	2940
CTTCCGCAAC	AGCATATGTA	GTTCCCGAAC	CACCAAATGG	ATCAAGAATT	AAACTATCTT	3000
TATTAGATGA	AGATAAAATT	ATTTTTTTAA	GCAATTCTAC	TGGCTTTTGC	GTAGGGTGAA	3060
TACTTCTTTC	CCAAGAACCA	TTTGAAATTG	TGGGAATCTC	CAAAACATCT	TTTGGCTTAG	3120

CTCCTAATGG GTTTGGCTCC CAAATATATT GCTTTTTTGA GTTCGAATAT TGCGAAGATT	3180
CGGCCTGGGT TCTTTGTGGA TATTTAACTG TATGCTCATT ATACGGGATT CGTGCCTCAT	3240
CAATATTAAA AATAAAATTT TTAGATTTTC TTAATAACAG TATACTTTCG TGTGAACGTC	3300
CCCAATCTTT ACCTAAATTT GCCTTGTTTC TATAGAACCA AATCAACCAT TTACAACTGT	3360
GAAAAATATTT TGAAGTGATA AATTTTATGT CTGCCAGAAT TTCTGAAAAG CCACAAACAT	3420
ATAAACTGCC ATTATCTTTT AAAACTCTAT GAGCTTCCAT TATCCATTCT TTACTCCATT	3480
CGAGATATTC ATTTTGAGAA GAAAAAATAT CCCACTCTGC CTTTTTAATG TTATAAGGTG	3540
GATCTGCAAA AATTAAATCC ACAGAATTAC TCTCTAATTT TCTTAAAAAA TCAATAGCAT	3600
CAACATTGAA AAGTGAACCG TTTTTTGAAA TAAAAAATGG TTTAAGCTCG ATTTCCGAAT	3660
AAAGTTTTAA TTTTGGTATA TAACTGTAAT TATCAAACGC TATTTTCATTC ACAAATGAAT	3720
CAATCTGCTG TTGTGTATAA ACCCTGTAAT TATTAATAGG ATGTCTTAAA CTTTTGAATT	3780
TTCCAGAATT ATCCCATCTT CCTTAATGTC TCAGAGTTAA CATCTAATAA TTTGCGCGCT	3840
TCTTTTATTG ATAAATAATC ATCCATATCT TACACAACAT TACACAAGTT TATACAGCAA	3900
ATATAAATAT TTTTATACA TTGTAAAAAT TTTATTTACT TTTATTTTGT TCAATTGTCT	3960
CAATAAATAG TTAATCGAAA TACATTTTGA ATATGATAAA ATTGACTCCA ACAAATCTAA	4020
CACAATGACA TTAAAACCAA TAAAAACGGA AGAAGATTAC AATCAGGTTT TAGAAAGACT	4080
TTCACAAATT TTCGACGCTA AACCAAATAC CAAAGATGGA GATGAATTGG GAAATCTTGG	4140
GAATTC	4146

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTTAGGTGA CACTATAGAA TAC

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAGCTCGAGT CTGATGACGA AGCTTGACTG ACTGAGATCA GCTTGCAAC

49

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGAGATTT AGGTGACACT ATAGAATACA AGCTT

35

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCGAGATTT AGGTGACACT ATAGAATACG GAATTGTGAG CGGATAACAA TTCCAAGCTT

60